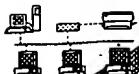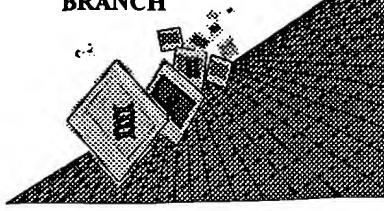S Foley

8 1309

RAW SEQUENCE LISTING
ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: _09/500,904_

Source: _1648_

Date Processed by STIC: _5/3/2001_

RECEIVED

MAY 1 6 2001

TECH CENTER 1600/2900

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:
1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY
FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.
PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)
PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.
Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO).
Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:
http://www.uspto.gov/web/offices/pac/checker

Raw Sequence Listing Error Summary

<u>ERROR DETECTED</u> <u>SUGGESTED CORRECTION</u>   SERIAL NUMBER: _09/500,904_

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

1 _____ Wrapped Nucleics
The number/text at the end of each line "wrapped" down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

2 _____ Wrapped Aminos
The amino acid number/text at the end of each line "wrapped " down to the next line.
This may occur if your file was retrieved in a word processor after creating it.
Please adjust your right margin to .3, as this will prevent "wrapping".

3 _____ Incorrect Line Length
The rules require that a line not exceed 72 characters in length. This includes spaces.

4 _____ Misaligned Amino Acid Numbering
The numbering under each 5th amino acid is misaligned. This may be caused by the use of tabs
between the numbering. It is recommended to delete any tabs and use spacing between the numbers.

5 _____ Non-ASCII
This file was not saved in ASCII (DOS) text, as required by the Sequence Rules.
Please ensure your subsequent submission is saved in ASCII text so that it can be processed.

6 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's which represented more than one residue.
As per the rules, each n or Xaa can only represent a single residue.
Please present the maximum number of each residue having variable length and
indicate in the (ix) feature section that some may be missing.

7 _____ PatentIn ver. 2.0 "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid
sequence(s) _____. Normally, PatentIn would automatically generate this section from the
previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section
to the subsequent amino acid sequence. **This applies primarily to the mandatory <220>-<223>
sections for Artificial or Unknown sequences.**

8 _____ Skipped Sequences (OLD RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X:
(i) SEQUENCE CHARACTERISTICS:(Do not insert any headings under "SEQUENCE CHARACTERISTICS")
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X:
This sequence is intentionally skipped

Please also adjust the "(iii) NUMBER OF SEQUENCES:" response to include the skipped sequence(s).

9 _____ Skipped Sequences (NEW RULES)
Sequence(s) _____ missing. If intentional, please use the following format for each skipped sequence.
<210> sequence id number
<400> sequence id number
000

10 _____ Use of n's or Xaa's (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Use of <220> to <223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

11 _____ Use of "Artificial" (NEW RULES)
Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules.
Valid response is Artificial Sequence.

12 _____ Use of <220>Feature (NEW RULES)
Sequence(s) _____ are missing the <220>Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213>ORGANISM is "Artificial Sequence" or "Unknown"
Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)   (Sec. 1.823 of new Rules)

13 _____ PatentIn ver. 2.0 "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted
file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing).
Instead, please use "File Manager" or any other means to copy file to floppy disk.

AMC - Biotechnology Systems Branch - 4/06/2001

RAW SEQUENCE LISTING   DATE: 05/03/2001
PATENT APPLICATION: US/09/500,904   TIME: 16:23:40

Input Set : A:\Om161ci1.app
Output Set: N:\CRF3\05032001\I500904.raw

**Does Not Comply
Corrected Diskette Needed**

```
 3 <110> APPLICANT: Harley, John B.
 4    .  James, Judith A.
 5       Kaufman, Kenneth M.
 7 <120> TITLE OF INVENTION: Diagnostics and Therapy of Epstein-Barr Virus in
 8       Autoimmune Disorders
10 <130> FILE REFERENCE: OMRF 161 CIP
12 <140> CURRENT APPLICATION NUMBER: 09/500,904
13 <141> CURRENT FILING DATE: 2000-02-09
15 <160> NUMBER OF SEQ ID NOS: 113
17 <170> SOFTWARE: PatentIn Ver. 2.1
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 7
21 <212> TYPE: PRT
22 <213> ORGANISM: Artificial Sequence
24 <220> FEATURE:
25 <223> OTHER INFORMATION: Description of Artificial Sequence: Epstein-Barr
26       virus Nuclear Antigen-1 Protein
28 <400> SEQUENCE: 1
29 Pro Pro Pro Gly Arg Arg Pro
30    1               5
33 <210> SEQ ID NO: 2
34 <211> LENGTH: 8
35 <212> TYPE: PRT
36 <213> ORGANISM: Artificial Sequence
38 <220> FEATURE:
39 <223> OTHER INFORMATION: Description of Artificial Sequence: Epstein-Barr
40       virus Nuclear Antigen-1 Protein
42 <400> SEQUENCE: 2
43 Gly Arg Gly Arg Gly Arg Gly Gly
44    1               5
47 <210> SEQ ID NO: 3
48 <211> LENGTH: 7
49 <212> TYPE: PRT
50 <213> ORGANISM: Artificial Sequence
52 <220> FEATURE:
53 <223> OTHER INFORMATION: Description of Artificial Sequence: Epstein-Barr
54       virus Nuclear Antigen-1 Protein
56 <400> SEQUENCE: 3
57 Arg Gly Arg Gly Arg Glu Lys
58    1               5
61 <210> SEQ ID NO: 4
62 <211> LENGTH: 8
63 <212> TYPE: PRT
64 <213> ORGANISM: Artificial Sequence
66 <220> FEATURE:
67 <223> OTHER INFORMATION: Description of Artificial Sequence: Octapeptide
69 <400> SEQUENCE: 4
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give source of genetic material - (see circled portion of item 12 on Era Summary Sheet) 5/3/01

```
70  Pro Pro Pro Gly Met Arg Pro Pro
71    1               5
74  <210> SEQ ID NO: 5
75  <211> LENGTH: 8
76  <212> TYPE: PRT
77  <213> ORGANISM: Artificial Sequence
79  <220> FEATURE:
80  <223> OTHER INFORMATION: Description of Artificial Sequence: Octapeptide
82  <400> SEQUENCE: 5
83  Pro Pro Pro Gly Ile Arg Gly Pro
84    1               5
87  <210> SEQ ID NO: 6
88  <211> LENGTH: 8
89  <212> TYPE: PRT
90  <213> ORGANISM: Artificial Sequence
92  <220> FEATURE:
93  <223> OTHER INFORMATION: Description of Artificial Sequence: Octapeptide
95  <400> SEQUENCE: 6
96  Pro Ala Pro Gly Met Arg Pro Pro
97    1               5
100 <210> SEQ ID NO: 7
101 <211> LENGTH: 24
102 <212> TYPE: PRT
103 <213> ORGANISM: Artificial Sequence
105 <220> FEATURE:
106 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide from
107       Epstein-Barr virus Nuclear Antigen-1
109 <400> SEQUENCE: 7
110 Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala Gly Ala
111   1               5                   10                  15
113 Gly Ala Gly Ala Gly Ala Gly Ala
114             20
117 <210> SEQ ID NO: 8
118 <211> LENGTH: 8
119 <212> TYPE: PRT
120 <213> ORGANISM: Artificial Sequence
122 <220> FEATURE:
123 <223> OTHER INFORMATION: Description of Artificial Sequence: Octapeptide
125 <400> SEQUENCE: 8
126 Pro Pro Pro Gly Met Arg Gly Pro
127   1               5
130 <210> SEQ ID NO: 9
131 <211> LENGTH: 26
132 <212> TYPE: PRT
133 <213> ORGANISM: Artificial Sequence
135 <220> FEATURE:
136 <223> OTHER INFORMATION: Description of Artificial Sequence: Peptide
138 <400> SEQUENCE: 9
139 Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg Gly Arg
```

```
140    1              5              10              15
142 Gly Arg Gly Arg Gly Gly Pro Arg Arg Arg
143              20              25
146 <210> SEQ ID NO: 10
147 <211> LENGTH: 9
148 <212> TYPE: PRT
149 <213> ORGANISM: Artificial Sequence
151 <220> FEATURE:
152 <223> OTHER INFORMATION: Description of Artificial Sequence: Phage
154 <400> SEQUENCE: 10
155 Gly Pro Pro Pro Gly Met Arg Pro Pro
156    1              5
159 <210> SEQ ID NO: 11
160 <211> LENGTH: 7
161 <212> TYPE: PRT
162 <213> ORGANISM: Artificial Sequence
164 <220> FEATURE:
165 <223> OTHER INFORMATION: Description of Artificial Sequence: Phage
167 <400> SEQUENCE: 11
168 Ser Pro Leu Ser Thr Leu Leu
169    1              5
172 <210> SEQ ID NO: 12
173 <211> LENGTH: 7
174 <212> TYPE: PRT
175 <213> ORGANISM: Artificial Sequence
177 <220> FEATURE:
178 <223> OTHER INFORMATION: Description of Artificial Sequence: Phage
180 <400> SEQUENCE: 12
181 Lys Ile Gly Phe Pro His Ile
182    1              5
185 <210> SEQ ID NO: 13
186 <211> LENGTH: 7
187 <212> TYPE: PRT
188 <213> ORGANISM: Artificial Sequence
190 <220> FEATURE:
191 <223> OTHER INFORMATION: Description of Artificial Sequence: Phage
193 <400> SEQUENCE: 13
194 Ile Pro Arg Pro Leu Asp Tyr
195    1              5
198 <210> SEQ ID NO: 14
199 <211> LENGTH: 7
200 <212> TYPE: PRT
201 <213> ORGANISM: Artificial Sequence
203 <220> FEATURE:
204 <223> OTHER INFORMATION: Description of Artificial Sequence: Phage
206 <400> SEQUENCE: 14
207 Met Lys Leu Lys His Pro Pro
208    1              5
211 <210> SEQ ID NO: 15
```

```
212 <211> LENGTH: 7
213 <212> TYPE: PRT
214 <213> ORGANISM: Artificial Sequence
216 <220> FEATURE:
217 <223> OTHER INFORMATION: Description of Artificial Sequence: Phage
219 <400> SEQUENCE: 15
220 Ile Leu Pro Pro Pro Gly Tyr
221   1           5
224 <210> SEQ ID NO: 16
225 <211> LENGTH: 7
226 <212> TYPE: PRT
227 <213> ORGANISM: Artificial Sequence
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Description of Artificial Sequence: Phage
232 <400> SEQUENCE: 16
233 Ala Val Ile His Arg Pro Pro
234   1           5
237 <210> SEQ ID NO: 17
238 <211> LENGTH: 7
239 <212> TYPE: PRT
240 <213> ORGANISM: Artificial Sequence
242 <220> FEATURE:
243 <223> OTHER INFORMATION: Description of Artificial Sequence: Phage
245 <400> SEQUENCE: 17
246 Ala Leu Ile Gln Arg Pro Pro
247   1           5
250 <210> SEQ ID NO: 18
251 <211> LENGTH: 7
252 <212> TYPE: PRT
253 <213> ORGANISM: Artificial Sequence
255 <220> FEATURE:
256 <223> OTHER INFORMATION: Description of Artificial Sequence: Phage
258 <400> SEQUENCE: 18
259 Val Pro Leu Thr Val Leu Leu
260   1           5
263 <210> SEQ ID NO: 19
264 <211> LENGTH: 6
265 <212> TYPE: PRT
266 <213> ORGANISM: Artificial Sequence
268 <220> FEATURE:
269 <223> OTHER INFORMATION: Description of Artificial Sequence: Phage
271 <400> SEQUENCE: 19
272 Ser Pro Pro Glu Leu Lys
273   1           5
276 <210> SEQ ID NO: 20
277 <211> LENGTH: 7
278 <212> TYPE: PRT
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/500,904

DATE: 05/03/2001
TIME: 16:23:40

Input Set : A:\Om161ci1.app
Output Set: N:\CRF3\05032001\I500904.raw

```
282 <223> OTHER INFORMATION: Description of Artificial Sequence: Phage
284 <400> SEQUENCE: 20
285 Lys Phe Leu Ala Pro Leu Gln
286   1               5
289 <210> SEQ ID NO: 21
290 <211> LENGTH: 18
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
297 <400> SEQUENCE: 21
298 ccagaggtaa gtggactt                                          18
301 <210> SEQ ID NO: 22
302 <211> LENGTH: 18
303 <212> TYPE: DNA
304 <213> ORGANISM: Artificial Sequence
306 <220> FEATURE:
307 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
309 <400> SEQUENCE: 22
310 gaccggtgcc ttcttagg                                          18
313 <210> SEQ ID NO: 23
314 <211> LENGTH: 58
315 <212> TYPE: DNA
316 <213> ORGANISM: Artificial Sequence
318 <220> FEATURE:
319 <223> OTHER INFORMATION: Description of Artificial Sequence: Probe
321 <400> SEQUENCE: 23
322 aagacgattc gggttgtgag gtggtgtggg tccgtgtgtg atgtgtgtgg gtgggcag   58
325 <210> SEQ ID NO: 24
326 <211> LENGTH: 32
327 <212> TYPE: PRT
328 <213> ORGANISM: Artificial Sequence
330 <220> FEATURE:
331 <223> OTHER INFORMATION: Description of Artificial Sequence: Octapeptide
332        from Epstein-Barr virus Nuclear Antigen-1
334 <400> SEQUENCE: 24
335 Gly Gly Ser Gly Pro Gln Arg Arg Gly Gly Asp Asn His Gly Arg Gly
336   1               5                  10                  15
338 Arg Gly Arg Gly Arg Gly Arg Gly Gly Gly Arg Pro Gly Ala Pro Gly
339              20                  25                  30
345 <210> SEQ ID NO: 25
346 <211> LENGTH: 20
347 <212> TYPE: PRT
348 <213> ORGANISM: Artificial Sequence
350 <220> FEATURE:
351 <223> OTHER INFORMATION: Description of Artificial Sequence: Octapeptide
352        from Epstein-Barr virus Nuclear Antigen-1
354 <400> SEQUENCE: 25
355 Gly Gly Ser Gly Ser Gly Pro Arg His Arg Asp Gly Val Arg Arg Pro
```

Please Note:
**Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.**

VERIFICATION SUMMARY
PATENT APPLICATION: US/09/500,904

DATE: 05/03/2001
TIME: 16:23:41

Input Set : **A:\Om161cil.app**
Output Set: **N:\CRF3\05032001\I500904.raw**

```
L:1124 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:80
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:83
L:1217 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:86
L:1261 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:89
L:1302 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:91
```

NOTICE TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE SEQUENCE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant must file the items indicated below within the time period set the Office action to which the Notice is attached to avoid abandonment under 35 U.S.C. § 133 (extensions of time may be obtained under the provisions of 37 CFR 1.136(a)).

The nucleotide and/or amino acid sequence disclosure contained in this application does not comply with the requirements for such a disclosure as set forth in 37 C.F.R. 1.821 - 1.825 for the following reason(s):

☒ 1. This application clearly fails to comply with the requirements of 37 C.F.R. 1.821-1.825. Applicant's attention is directed to these regulations, published at 1114 OG 29, May 15, 1990 and at 55 FR 18230, May 1, 1990.

☐ 2. This application does not contain, as a separate part of the disclosure on paper copy, a "Sequence Listing" as required by 37 C.F.R. 1.821(c).

☒ 3. A copy of the "Sequence Listing" in computer readable form has not been submitted as required by 37 C.F.R. 1.821(e).

☐ 4. A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 C.F.R. 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing."

☐ 5. The computer readable form that has been filed with this application has been found to be damaged and/or unreadable as indicated on the attached CRF Diskette Problem Report. A Substitute computer readable form must be submitted as required by 37 C.F.R. 1.825(d).

☐ 6. The paper copy of the "Sequence Listing" is not the same as the computer readable from of the "Sequence Listing" as required by 37 C.F.R. 1.821(e).

☐ 7. Other: _____

Applicant Must Provide:

☒ An initial or substitute computer readable form (CRF) copy of the "Sequence Listing".

☐ An initial or substitute paper copy of the "Sequence Listing", as well as an amendment directing its entry into the specification.

☒ A statement that the content of the paper and computer readable copies are the same and, where applicable, include no new matter, as required by 37 C.F.R. 1.821(e) or 1.821(f) or 1.821(g) or 1.825(b) or 1.825(d).

For questions regarding compliance to these requirements, please contact:
For Rules Interpretation, call (703) 308-4216
For CRF Submission Help, call (703) 308-4212
PatentIn Software Program Support (SIRA)
        Technical Assistance.......................................703-287-0200
        To Purchase PatentIn Software.......................703-306-2600
PLEASE RETURN A COPY OF THIS NOTICE WITH YOUR RESPONSE